

us-10-063-557-50.rag

ON N-PSDB; AAC66135.

disease associated gene useful for diagnosing treating and renal disorders, is uromodulin, NKCC2, NCCT, aldolase B, IL, PDZK1, NPT1, calbindin, Kininogen or CIC-Kb -

re 35-36; 36pp; English.

des AAC66131-C66139 represent human kidney disease genes. Proteins AAY85678-Y85680 represent human kidney disease proteins. The polynucleotides have nephrotropic and cytostatic re polynucleotides, encoded proteins and pharmaceutical containing them are useful for diagnosing, prognosis, preventing renal disorders such as Bartter's syndrome,ndrome, autosomal dominant polycystic kidney disease and sis. The genes and proteins are also useful for identifying that are associated with a specific disease, regulatory cellular compartment, cell type, tissue type or species useful in diagnosis, prognosis, treatment and evaluation of renal diseases for e.g. renal amyloidosis, hypertension, steronism, Addison's disease, renal failure, arthritis, chronic glomerulonephritis, tubulointerstitial ystic disorders and dysplastic malformations, inherited renal disease (PRD), medullary cystic disease, medullary y and tubular dysplasia. Alport's syndrome, non-renal they adenocarcinoma, metastatic renal carcinoma, multiple nephrotropic disorders.

9 AA;

100.0%; Score 461; DB 21; Length 89;
larity 100.0%; Pred. No. 1.2e-50;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

VTALLLAGLTALEANDPFANKDDPFYDWKNLQSLICGGLIATAGIAVLGSK 60
VTALLLAGLTALEANDPFANKDDPFYDWKNLQSLICGGLIATAGIAVLGSK 60

KSSQKQHSVPPEKAIPITPGSATTC 89
KSSQKQHSVPPEKAIPITPGSATTC 89

ndard; Protein; 89 AA.

(first entry)

peptide containing protein HSPB-35 SEQ ID NO:35.

1 peptide-containing protein; HSPB; diagnosis; cancer;
; cardiovascular disease; anticancer; anti-inflammatory;
i; nontropic; neuroprotective; cardiovascular; hepatotropic;
c; gene therapy; cell proliferation; neurological disorder;
disorder; developmental disorder; arteriosclerosis;
soriasis; acquired immune deficiency syndrome; anaemia;
n's disease; infection; Alzheimer's disease; schizophrenia;
disease; Huntington's diseases; ovulatory defect;
trophy.

A2.

99WO-US14484.

98US-0090762.
98US-0094983.
98US-0102686.

PR 11-DEC-1998; 98US-0112129.
XX (INCY-) INCYTE PHARM INC.
XX
XX
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn I
PI Akerbloom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hill;
PI Bandman O;
XX
XX WPI; 2000-160673/14.
DR N-PSDB; AAZ98143.

XX New human signal peptide-containing proteins useful in treatment
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease -

PS Claim 1; Page 182; 327pp; English.

XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent
CC human signal peptide-containing proteins HSPB-1 to HSPB-134. HSPB
CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepat
CC neuroprotective, cardiovascular and antiasthmatic activities, ar
CC be used in gene therapy. HSPBs can be used to treat or prevent c
CC associated with decreased activity or function of HSPB. Antagon
CC HSPB are used to treat or prevent disorders associated with inc
CC activity or function of HSPB. Such diseases include cell prolif
CC (including cancer), inflammation, cardiovascular, neurological
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaem
CC asthma, Crohn's disease, microbial or other infections, congest
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy).
CC nucleic acids can be used for the recombinant production of HSPB
CC detecting HSPB in standard hybridisation and amplification assa
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related
CC or genetic variations, and for chromosomal mapping. HSPB are als
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagn
CC monitor, HSPB-related diseases (in usual immunoassays), as ther
CC antagonists, in competitive drug screens, and for purification c
CC from natural sources.

XX Sequence 89 AA;

Query Match 100.0%; Score 461; DB 21; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0;

QY 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWKNLQSLICGGLIATAGIAF
Db 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWKNLQSLICGGLIATAGIAF

QY 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89
Db 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89

RESULT 3

AAY66705
ID AAY66705 standard; protein; 89 AA.

XX AAY66705;

XX 05-APR-2000 (first entry)

XX Membrane-bound protein PRO1069.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE 1
KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX Homo sapiens.

XX WO9963088-A2.

99WO-US:2252.
 98US-0087607.
 98US-0087609.
 98US-0087755.
 98US-0087827.
 98US-0088021.
 98US-0088025.
 98US-0088028.
 98US-0088029.
 98US-0088030.
 98US-0088033.
 98US-0088326.
 98US-0088167.
 98US-0088202.
 98US-0088212.
 98US-0088217.
 98US-0088655.
 98US-0088722.
 98US-0088730.
 98US-0088734.
 98US-0088738.
 98US-0088740.
 98US-0088741.
 98US-0088742.
 98US-0088810.
 98US-0088811.
 98US-0088824.
 98US-0088825.
 98US-0088826.
 98US-0088858.
 98US-0088861.
 98US-0088863.
 98US-0088876.
 98US-0089090.
 98US-0089105.
 98US-0089440.
 98US-0089512.
 98US-0089514.
 98US-0089518.
 98US-0089538.
 98US-0089598.
 98US-0089599.
 98US-0089600.
 98US-0089653.
 98US-0089801.
 98US-0089907.
 98US-0089908.
 98US-0089947.
 98US-0089948.
 98US-0089952.
 98US-0090246.
 98US-0090252.
 98US-0090254.
 98US-0090349.
 98US-0090355.
 98US-0090429.
 98US-0090431.
 98US-0090435.
 98US-0090444.
 98US-0090445.
 98US-0090461.
 98US-0090472.
 98US-0090535.
 98US-0090538.
 98US-0090540.
 98US-0090557.
 98US-0090676.
 98US-0090678.
 98US-0090688.

PR 25-JUN-1998; 98US-0090690.
 PR 25-JUN-1998; 98US-0090691.
 PR 25-JUN-1998; 98US-0090694.
 PR 25-JUN-1998; 98US-0090695.
 PR 25-JUN-1998; 98US-0090696.
 PR 26-JUN-1998; 98US-0090862.
 PR 26-JUN-1998; 98US-0090863.
 PR 01-JUL-1998; 98US-0091358.
 PR 01-JUL-1998; 98US-0091360.
 PR 01-JUL-1998; 98US-0091544.
 PR 02-JUL-1998; 98US-0091478.
 PR 02-JUL-1998; 98US-0091486.
 PR 02-JUL-1998; 98US-0091519.
 PR 02-JUL-1998; 98US-0091626.
 PR 02-JUL-1998; 98US-0091628.
 PR 02-JUL-1998; 98US-0091633.
 PR 02-JUL-1998; 98US-0091646.
 PR 02-JUL-1998; 98US-0091673.
 PR 07-JUL-1998; 98US-0091978.
 PR 07-JUL-1998; 98US-0091982.
 PR 09-JUL-1998; 98US-0092182.
 PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
 PR 04-AUG-1998; 98US-0095285.
 PR 04-AUG-1998; 98US-0095301.
 PR 04-AUG-1998; 98US-0095302.
 PR 04-AUG-1998; 98US-0095318.
 PR 04-AUG-1998; 98US-0095321.
 PR 04-AUG-1998; 98US-0095325.
 PR 10-AUG-1998; 98US-0095916.
 PR 10-AUG-1998; 98US-0095929.
 PR 10-AUG-1998; 98US-0096012.
 PR 11-AUG-1998; 98US-0096143.
 PR 11-AUG-1998; 98US-0096146.
 PR 12-AUG-1998; 98US-0096323.
 PR 17-AUG-1998; 98US-0096757.
 PR 17-AUG-1998; 98US-0096766.
 PR 17-AUG-1998; 98US-0096768.
 PR 17-AUG-1998; 98US-0096773.
 PR 17-AUG-1998; 98US-0096791.
 PR 17-AUG-1998; 98US-0096867.
 PR 17-AUG-1998; 98US-0096891.
 PR 17-AUG-1998; 98US-0096894.
 PR 17-AUG-1998; 98US-0096895.
 PR 17-AUG-1998; 98US-0096897.
 PR 18-AUG-1998; 98US-0096949.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096959.
 PR 18-AUG-1998; 98US-0096960.
 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
 PR 24-AUG-1998; 98US-0097661.
 PR 26-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 26-AUG-1998; 98US-0098014.
 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.
 XX
 PA (GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 Wood WI, Yuan J;
 PI

2883/06.
15045.

and proteins and related nucleotide sequences -

g 180; 822pp; English.

in provides membrane-bound PRO polypeptides and des encoding them. The PRO sequences of the invention were based on extracellular domain homology screening. The PRO ve homology with proteins including LDL receptors, TIE various enzymes. The membrane-bound proteins and receptor e useful as pharmaceutical and diagnostic agents. Receptor ns, for instance, can be used as therapeutic agents to block and interactions. The membrane-bound proteins can also be screening of potential peptide or small molecule inhibitors ant receptor/ligand interaction. The PRO encoding sequences s hybridization probes, in chromosome and gene mapping and in on of antisense RNA and DNA. PRO nucleic acid sequences useful for the preparation of PRO polypeptides, especially nt techniques.

9 AA;

100.0%; Score 461; DB 21; Length 89;

larity 100.0%; Pred. No. 1.2e-50;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

VTLLALLAGLTALANDPFANKDDPFYDWNKQLQSLGICGGLAAGTAAVLGSK 60

VTLLALLAGLTALANDPFANKDDPFYDWNKQLQSLGICGGLAAGTAAVLGSK 60

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

KSSQKQHSVPPEKAIPITPGSATTC 89

29-MAR-2000; 2000US-191032P.
29-MAR-2000; 2000US-191053P.
30-MAR-2000; 2000WO-US08439.
04-APR-2000; 2000US-194449P.
04-APR-2000; 2000US-194647P.
11-APR-2000; 2000US-195975P.
11-APR-2000; 2000US-196000P.
11-APR-2000; 2000US-196187P.
11-APR-2000; 2000US-196690P.
11-APR-2000; 2000US-196820P.
18-APR-2000; 2000US-198121P.
18-APR-2000; 2000US-198585P.
25-APR-2000; 2000US-19397P.
25-APR-2000; 2000US-195550P.
25-APR-2000; 2000US-19654P.
03-MAY-2000; 2000US-201516P.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
05-JUN-2000; 2000US-209832P.
28-JUL-2000; 2000WO-US20710.
22-AUG-2000; 2000US-0644848.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurr Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.

N-PSDB; AAS46024.

Novel nucleic acids encoding PRO polypeptides, used to diagnose presence of tumours, such as prostate and breast tumours, in man to screen for modulators of the compounds -

Claim 11; Fig 200; 774pp; English.

Sequences AAU29324-AAU29328 represent PRO polypeptides of the in The PRO polypeptides and their associated nucleic acids can be u detect the presence of a tumour in a mammal by comparing the lev expression of a PRO polypeptide in a test sample of cells from t and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, CC and rabbits but are preferably human. The polypeptides can be us stimulate tumour necrosis factor (TNF) alpha release from human CC when contacted with it. A specific polypeptide can be used to st the proliferation or differentiation of chondrocyte cells. The P proteins can be used to determine the presence of tumours and al susceptibility to tumour development, particularly adrenal, lung breast, prostate, rectal, cervical, or liver tumours, in mammali CC subjects. The oligonucleotide probes specific for the PRO nuclei CC can be used for genetic analysis of individuals with genetic dis

Sequence 89 AA;

Query Match 100.0%; Score 461; DB 22; Length 89;

Best Local Similarity 100.0%; Pred. No. 1.2e-50;

Matches 89; Conservative 0; Mismatches 0; Indels 0; (

QY 1 MERVTLALLLAGLTALANDPFANKDDPFYDWNKQLQSLGICGGLAAGTAA

Db 1 MERVTLALLLAGLTALANDPFANKDDPFYDWNKQLQSLGICGGLAAGTAA

QY 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89

Db 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89

ard; Protein; 89 AA.

(first entry)

rotein; mapping.

2.

2000WO-US23328.

99WO-US20111.
99WO-US21090.
99US-0169495.
99US-0170262.
2000US-0175481.
2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
2000WO-US05601.
2000US-0187202.
2000US-0193397.
2000WO-US14042.
2000US-0209832.

TECH INC.

Ivaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Gurney AL, Watanabe CK, Wood WI;

260/18.
382.

nucleic acids encoding PRO polypeptides, useful in
logy, including use as hybridization probes, and in
i gene mapping. -

50; 278pp; English.

sequence is a human PRO polypeptide (secreted and
). The PRO protein, and PRO agonists, PRO antagonists or
odies are useful for preparation of a medicament useful in
of a condition which is responsive to the PRO protein,
agonists or anti-PRO antibodies. The PRO protein may also be
lecular weight markers for protein electrophoresis. The PRO
e has applications in molecular biology, including use as
probes, and in chromosome and gene mapping.

AA:

100.0%; Score 461; DB 22; Length 89;
arity 100.0%; Pred. NO. 1.2e-50;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

TLALLLAGLTALENDPPFANKDDPFYDWNKQLSLGGLIAGIAVLGSK 60
TLALLLAGLTALENDPPFANKDDPFYDWNKQLSLGGLIAGIAVLGSK 60
3SQKQHSVPVPEKAIPITPGSATTC 89
3SQKQHSVPVPEKAIPITPGSATTC 89

RESULT 6
AAB65228
ID AAB65228 standard; Protein; 89 AA.
XX
AC AAB65228;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1069 (JNQ526) protein sequence SEQ ID NO:262.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue tyf
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0145698.
PR 17-AUG-1999; 99US-0146222.
PR 15-SEP-1999; 99US-0149396.
PR 13-SEP-1999; 99WO-US21090.
PR 08-OCT-1999; 99WO-US21547.
PR 30-NOV-1999; 99US-0158663.
PR 01-DEC-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 03-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AU, Baker KP, Botstein D, Desnovers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godows
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44191.
XX
PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
PS Claim 12; Fig 180; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane
CC proteins. The PRO proteins have cytostatic activity. The PRO prot
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nuc
CC sequences, and their fragments, can be used as hybridisation prob
CC chromosomal and gene mapping, and in the generation of anti-sense
CC and DNA. They may also be used to produce transgenic animals whic
CC used to develop and screen therapeutically useful reagents. The P
CC nucleotide and protein sequence can be used for tissue typing and

PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 31-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.

dard; Protein; 89 AA.

(first entry)
protein.
ecrated; transmembrane; cytostatic; TNF-alpha; blood;
is factor alpha release; chondrocyte cell; proliferation;
on; tumour; Gene therapy.

A1.

2002US-0187600.
98WO-US19330.
98WO-US21141.
98WO-US25108.
99WO-US05028.
99WO-US10733.
99WO-US12252.
99WO-US20111.
99WO-US21090.
99WO-US28301.
99WO-US28551.
99WO-US31274.
2000WO-US00219.
2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
2000WO-US05004.
2000WO-US05601.
2000WO-US05841.
2000WO-US06884.
2000WO-US08439.
2000WO-US13705.
2000WO-US14042.
2000WO-US14941.
2000WO-US15264.
2000WO-US20710.
2000WO-US23328.
2000WO-US30952.
2000WO-US32678.
2000WO-US34956.
2001WO-US06520.
2001WO-US17800.
2001WO-US19692.
2001WO-US21066.
2001WO-US21735.
2001WO-US27099.
97US-059263P.
97US-059266P.
97US-062250P.
97US-063486P.
97US-063120P.
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97US-063540P.
97US-063541P.
97US-063544P.
97US-063564P.
97US-063734P.
97US-063870P.
97US-064103P.
97US-065311P.

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 98US-090246P.
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 98US-096897P.
 98US-096949P.
 98US-096959P.
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 98US-097952P.
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 98US-098803P.
 98US-098821P.
 98US-098843P.
 98US-099602P.
 98US-099741P.
 98US-099754P.
 98US-099763P.
 98US-099812P.

arity 100.0%; Score 461; DB 24; Length 89;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAALLAGLTALEANDPFANKDDPFYDWNKQLQSLGICGLLAIAAGIAVLGSK 60

TTAALLAGLTALEANDPFANKDDPFYDWNKQLQSLGICGLLAIAAGIAVLGSK 60

SSQKHSPVPEKAIPLITPGSATTG 89

SSQKHSPVPEKAIPLITPGSATTG 89

ABU71530.

ID ABU71530 standard; Protein; 89 AA.

XX

AC ABU71530;

XX

DT 10-JUN-2003 (first entry)

XX

DE Human secreted polypeptide PRO1069.

XX

KW Human; gene therapy; tumour; cancer.

XX

OS Homo sapiens.

XX

PN US2003013855-A1.

XX

PD 16-JAN-2003.

XX

PF 03-MAY-2002; 2002US-0063616.

XX

PR 30-DEC-1998; 98KR-0062142.

PR

PR 08-MAR-1999; 99WO-US05028.

PR

PR 14-MAY-1999; 99WO-US10733.

PR

PR 30-DEC-1999; 99WO-US31274.

PR

PR 18-FEB-2000; 2000WO-US04341.

PR

PR 01-MAR-2000; 2000WO-US05601.

PR

PR 21-MAR-2000; 2000WO-US05841.

PR

PR 22-MAY-2000; 2000WO-US10402.

PR

PR 24-AUG-2000; 2000WO-US23328.

PR

PR 10-NOV-2000; 2000WO-US30873.

PR

PR 01-DEC-2000; 2000WO-US32678.

PR

PR 20-DEC-2000; 2000WO-US34956.

PR

PR 28-FEB-2001; 2001WO-US06520.

PR

PR 01-JUN-2001; 2001WO-US17800.

PR

PR 14-MAY-1999; 99US-0311832.

PR

PR 25-AUG-1999; 99US-0380137.

PR

PR 25-AUG-1999; 99US-0380138.

PR

PR 25-AUG-1999; 99US-0380139.

PR

PR 15-SEP-1999; 99US-0397342.

PR

PR 18-OCT-1999; 99US-0403297.

PR

PR 12-NOV-1999; 99US-0423844.

PR

PR 22-AUG-2000; 2000US-0644848.

PR

PR 18-SEP-2000; 2000US-0664610.

PR

PR 18-SEP-2000; 2000US-0665350.

PR

PR 08-NOV-2000; 2000US-0709238.

PR

PR 20-DEC-2000; 2000US-0747259.

PR

PR 22-MAR-2001; 2001US-0816744.

PR

PR 10-MAY-2001; 2001US-0854208.

PR

PR 30-MAY-2001; 2001US-0870574.

PR

PR 05-JUN-2001; 2001US-0874503.

PR

PR 29-JUN-2001; 2001US-0869599.

PR

PR 18-JUL-2001; 2001US-0908827.

PR

PR 06-DEC-2001; 2001US-0008867.

XX

PA (GETH) GENENTECH INC.

XX

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

PI

XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX

DR WPI; 2003-330485/31.

DR

DR N-PSDB; ACA58834.

XX

PT New isolated antibody specifically binding a PRO polypeptide, use

PT

PT for the preparation of a medicament for treating disorders with t

PT

PT aberrant expression or activity of the PRO polypeptide, such as t

PT

XX conditions and cancer

XX

PS Disclosure; Page 117; 406pp; English.

PS

XX The invention relates to an antibody that binds to a polypeptide

CC

sequence given in the specification. The methods and (containing antibodies that specifically bind a PRO of the present invention are useful for the preparation of a treatment of disorders associated with the aberrant activity of the PRO polypeptide, such as tumour conditions they can also be used to generate transgenic or knockout PRO polypeptides and screening of therapeutically useful PRO polypeptides and encoding nucleic acids can be used as markers for protein electrophoresis, chromosome and tissue typing. The PRO polypeptides are useful to enesis e.g wound healing; in the treatment of sports-related s, articular cartilage defects, osteoarthritis or rheumatoid abetes; hyperinsulinaemia and hypoinsulinaemia. The y be used in various diagnostic, competitive binding and/or tation assays. The present sequence represents the amino of a PRO polypeptide of the invention.

AA;

100.0%; Score 461; DB 24; Length 89;
arity 100.0%; Pred. No. 1.2e-50;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TLALLLAGLTALEANDPFANKDPPFYDWKNLQSLICGGLIAIAGIAVLSGK 60
TLALLLAGLTALEANDPFANKDPPFYDWKNLQSLICGGLIAIAGIAVLSGK 60

SSQKQHSVPPEKAIPITPGSATTC 89
|||
SSQKQHSVPPEKAIPITPGSATTC 89

lard; Protein; 89 AA.

(first entry)

creted and transmembrane protein PRO1069.

ed and transmembrane polypeptide;
oping; gene mapping; transgenic animal; knockout animal;
gent screening; chromosome identification; tissue typing;

A1.

002US-0063512.

001US-0006867.

TECH INC.

varoff E, Gerritsen ME, Goddard A, Godowski PJ;
Gurney AL, Watanabe CK, Wood WI;

84/31.
87.

and transmembrane PRO polypeptides and nucleic acid
ding the polypeptides, useful in gene therapy or
dicament for treating a condition that is responsive to
ptide or antibody -

g 50; 409pp; English.

describes novel isolated PRO polypeptides. The PRO

CC polypeptides or anti-PRO antibodies are useful in preparing a me
CC for treating a condition that is responsive to the PRO polypepti
CC antibody. The PRO nucleotide sequences may be used as hybridizat
CC probes in chromosome and gene mapping, or in generating antisens
CC and DNA. PRO nucleic acids are also useful in preparing PRO poly
CC in assays to identify other proteins or molecules involved in bi
CC reaction, to generate transgenic animals or knockout animals, wh
CC turn are useful in the development and screening of therapeutica
CC useful reagents, for chromosome identification, and tissue typin
CC PRO polypeptides and nucleic acid molecules are also useful in g
CC therapy, and as molecular weight markers for protein electrophor
CC purposes. The anti-PRO antibodies may be used in diagnostic assa
CC PRO, or for the affinity purification of PRO from recombinant ce
CC culture or natural sources. This is the amino acid sequence of a
CC human secreted and transmembrane PRO polypeptide.

XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 461; DB 24; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0; (

QY 1 NERVTLALLLAGLTALEANDPFANKDPPFYDWKNLQSLICGGLIAIAGIAA
DB 1 NERVTLALLLAGLTALEANDPFANKDPPFYDWKNLQSLICGGLIAIAGIAA

QY 61 CKYSSQKQHSVPPEKAIPITPGSATTC 89
|||

DB 61 CKYSSQKQHSVPPEKAIPITPGSATTC 89
|||

RESULT 11

ABU72133
ID ABU72133 standard; Protein; 89 AA.

XX AC ABU72133;

XX DT 13-JUN-2003 (first entry)

XX DE Human PRO polypeptide #25.

XX KW Human; PRO polypeptide; secreted and transmembrane protein;
XX XM anti-PRO antibody; diagnostic assay; gene expression.

XX OS Homo sapiens.

XX PN US2003023042-A1.

XX PD 30-JAN-2003.

XX PF 01-MAY-2002; 2002US-0063502.

XX PR 06-DEC-2001; 2001US-0006867.

XX PA (GETH) GENENTECH INC.

XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX DR WPI; 2003-331484/31.

XX DR N-PSDB; ACA63397.

XX PT Novel monoclonal antibody that binds to secreted and transmembran
XX PT polypeptide, useful for detecting and purifying the polypeptide a
XX PT also for treating conditions responsive to the antibody -
XX PS Disclosure; Fig 50; 408pp; English.

XX CC The present invention relates to the isolation of novel human PRO
XX CC polypeptides, and the polynucleotide sequences encoding them. The
XX CC PRO polypeptides are secreted and transmembrane proteins. The PRO
XX CC polypeptides and polynucleotides are useful for preparing a
XX CC medicament useful in the treatment of a condition responsive to

ibody. Anti-PRO antibodies are useful in diagnostic
PRO, by detecting its expression in specific cells,
serum, and for affinity purification of PRO from
cell culture or natural sources. ABU72109-ABU72192
are human PRO polypeptides of the invention.

39 AA;

100.0%; Score 461; DB 24; Length 89;

ilarity 100.0%; Pred. No. 1.2e-50;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RYTALLLLAGLTALANDPFANKDDPFYDWNKQLSLGGLIAGIAIAVLGSK 60

RYTALLLLAGLTALANDPFANKDDPFYDWNKQLSLGGLIAGIAIAVLGSK 60

KSSQKHSPVPEKAIPITPGSATTC 89

KSSQKHSPVPEKAIPITPGSATTC 89

ndard; Protein; 89 AA.

(first entry)

ed/transmembrane protein, SEQ ID 200.

secreted protein; transmembrane protein;
antiarthritic; osteopathic; adrenal tumour;
breast tumour; prostate tumour; rectal tumour;
liver tumour; TNF-alpha release; arthritis;
factor alpha; chondrocyte cell; bone disorder;
sorder; sports injury.

-Al.

2002US-0188767.

98WO-US19330.

98WO-US21141.

98WO-US25108.

99WO-US05028.

99WO-US10733.

99WO-US12252.

99WO-US20111.

99WO-US21090.

99WO-US28101.

99WO-US28551.

99WO-US31274.

2000WO-US00219.

2000WO-US04341.

2000WO-US04342.

2000WO-US04414.

2000WO-US05004.

2000WO-US05601.

2000WO-US05841.

2000WO-US06884.

2000WO-US08439.

2000WO-US13705.

2000WO-US14042.

2000WO-US14941.

2000WO-US15264.

2000WO-US20710.

2000WO-US23328.

2000WO-US30952.

01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-JUN-2001; 2001WO-US17800.
20-JUN-2001; 2001WO-US19692.
29-JUN-2001; 2001WO-US21066.
09-JUL-2001; 2001WO-US21735.
29-AUG-2001; 2001WO-US27099.
18-SEP-1997; 97US-059263P.
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17-OCT-1997; 97US-062250P.
21-OCT-1997; 97US-063486P.
24-OCT-1997; 97US-063120P.
24-OCT-1997; 97US-063121P.
28-OCT-1997; 97US-063540P.
28-OCT-1997; 97US-063541P.
28-OCT-1997; 97US-063544P.
28-OCT-1997; 97US-063564P.
29-OCT-1997; 97US-063734P.
31-OCT-1997; 97US-063870P.
31-OCT-1997; 97US-064103P.
13-NOV-1997; 97US-065311P.
21-NOV-1997; 97US-066120P.
24-NOV-1997; 97US-066466P.
11-DEC-1997; 97US-066772P.
12-DEC-1997; 97US-069335P.
17-DEC-1997; 97US-069435P.
18-DEC-1997; 97US-069870P.
10-MAR-1998; 97US-068017P.
11-MAR-1998; 97US-077450P.
11-MAR-1998; 97US-077632P.
20-MAR-1998; 98US-077649P.
20-MAR-1998; 98US-078886P.
27-MAR-1998; 98US-078939P.
27-MAR-1998; 98US-079684P.
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31-MAR-1998; 98US-080107P.
01-APR-1998; 98US-080194P.
01-APR-1998; 98US-080327P.
08-APR-1998; 98US-080333P.
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09-APR-1998; 98US-081070P.
15-APR-1998; 98US-081195P.
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21-APR-1998; 98US-082568P.
22-APR-1998; 98US-082569P.
28-APR-1998; 98US-082797P.
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06-MAY-1998; 98US-084366P.
07-MAY-1998; 98US-084414P.
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 98US-098014P.
 98US-098716P.
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 98US-098803P.

PR 02-SEP-1998; 98US-098821P.
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 PR 10-SEP-1998; 98US-099741P.
 Query Match 100.0%; Score 461; DB 24; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.2e-50;
 Matches 89; Conservative 0; Mismatches 0; Indels 0;
 QY 1 MERVTLALLLAGLTALEANDPPFANKDDPFYDWNKLNLOISGLICGLLAIAIAA
 Db 1 MERVTLALLLAGLTALEANDPPFANKDDPFYDWNKLNLOISGLICGLLAIAIAA
 QY 61 CKYSSQKQHSVPPEKAIPITPGSATTG 89
 Db 61 CKYSSQKQHSVPPEKAIPITPGSATTG 89
 RESULT 13
 ABU66001
 ID ABU66001 standard; Protein; 89 AA.
 XX AC ABU66001;
 XX DT 20-MAY-2003 (first entry)
 XX DE Novel human secreted and transmembrane protein PRO1069.
 KW Human; secreted protein; transmembrane protein; cytostatic;
 KW Gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
 KW adrenal tumour; lung tumour; colon tumour; breast tumour;
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
 XX OS Homo sapiens.
 XX PN US2003036157-A1.
 XX PD 20-FEB-2003.
 XX PF 02-JUL-2002; 2002US-0188769.
 XX PR 16-SEP-1998; 98WO-US19330.
 PR 07-OCT-1998; 98WO-US21141.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-MAR-1999; 99WO-US05028.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 13-SEP-1999; 99WO-US21090.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28551.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
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 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.

2001WO-US21066.
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2001WO-US27099.
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09:53:12 2004

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(first entry)

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16-AUG-2001; 2001US-0931836.
28-AUG-2001; 2001US-0941992.
04-SEP-2001; 2001US-0946374.
15-JAN-2002; 2002US-0052586.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurne
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-332039/31.
N-PSDB; ACA05799.

New secreted and transmembrane PRO polypeptides and nucleic acids
useful in gene therapy, in chromosome and gene mapping, as chromo
markers, in tissue typing, and in chromosome identification -

Claim 11; Fig 200; 706pp; English.

The invention discloses human nucleic acids encoding secreted and
transmembrane (PRO) polypeptides. Also disclosed is an antibody t
specifically binds to the PRO polypeptide, a method for stimulat
release of tumour necrosis factor alpha (TNF-alpha) from human bl
contacting the blood a PRO polypeptide, a method for stimulating
proliferation or differentiation of chondrocyte cells by contacti
cells with a PRO polypeptide, a method for detecting the presence
tumour in a mammal and an oligonucleotide probe derived from any
PRO nucleotide sequences. The nucleotide sequences are useful as
in chromosome and gene mapping, in generating antisense RNA and D
preparing PRO polypeptides by recombinant techniques and in gene
(e.g. for replacement of defective gene). The PRO polypeptides ar
as molecular weight markers for protein electrophoresis purposes,
chromosome identification, as chromosome markers, as therapeutic
for stimulating the release of TNF-alpha from human blood, for
stimulating the proliferation or differentiation of chondrocytes
detecting the presence of a tumour. The PRO polypeptides and nucl
acids may also be used diagnostically for tissue typing. The sequ
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(first entry)

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cytostatic; chromosome mapping; gene mapping;
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differentiation; chondrocyte proliferation; tumour.

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1.6	87	1	US-08-725-531-5	Sequence 5, Appl
1.6	87	2	US-08-738-127-5	Sequence 5, Appl
1.6	87	2	US-09-213-392-5	Sequence 5, Appl
1.6	87	2	US-09-083-661-5	Sequence 5, Appl
1.5	87	1	US-08-289-247B-4	Sequence 4, Appl
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1.0	92	4	US-09-247-155-120	Sequence 120, App
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1.4	92	2	US-09-213-392-3	Sequence 3, Appl
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1.4	95	1	US-08-725-531-1	Sequence 1, Appl
1.4	95	2	US-09-213-392-1	Sequence 1, Appl
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1.4	120	4	US-09-996-243-199	Sequence 199, App
1.0	69	4	US-09-149-476-606	Sequence 606, App
1.6	72	3	US-08-905-223-405	Sequence 405, App
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ALIGNMENTS

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; Patent No. 6277574
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; APPLICANT: Volkuth, Wayne
; APPLICANT: Klinger, Ted, M.
; APPLICANT: Azimzal, Yalda
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
; FILE REFERENCE: PB-0010 US
; CURRENT APPLICATION NUMBER: US/09/289,349
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 11
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RESULT 2
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; Sequence 262, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
```


critsen, Mary E.
idard, Audrey
owski, Paul J.
imaldi, J. Christopher
ney, Austin L.
avin, Ivar J.
ier, Mary A.
l, James
ni, Nicholas F.
y, Margaret Ann
ewart, Timothy A.
was, Daniel
tanabe, Colin K.
lliams, P. Mickey
od, William I.
ang, Zemin
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ON NUMBER: 60/092182
TE: 1998-07-09

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lication US/09724864

62
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ison, James G.
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11000.105003
TION NUMBER: US/09724,864
DATE: 2000-11-28
ON NUMBER: U.S. No. 6380362 60/171,678
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US-09-724-864-58

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; Sequence 5, Application US/08725531
; Patent No. 5756310
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08725,531
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0128 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; LIBRARY: GenBank
; CLONE: 951423
US-08-725-531-5

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Db 1 MEGITCAFLVLLAGLPVLEANGP-VDKGSPFYDWSLQGLGIFGGLCIAGIAN

○
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○
○

YKSSQKQ-HSPVPEKAIPITPGSA 86
 CKFGQKSGHH--PGETPPLITPGSA 85

lication US/08738127

655

ATION:

Bandman, Olga

Hawkins, Phillip R.

ENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG

QUENCES: 6

CE ADDRESS:

Incyte Pharmaceuticals, Inc.

174 Porter Drive

o Alto

US

4

DABLE FORM:

E: Diskette

IBM Compatible

SYSTEM: DOS

FastSEQ Version 1.5

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N NUMBER: US/08/738,127

E: Filed Herewith

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N NUMBER:

E:

NT INFORMATION:

lings, Lucy J.

ON NUMBER: 36,749

DOCKET NUMBER: PF-0141 US

ATION INFORMATION:

415-855-0555

415-845-4166

R SEQ ID NO: 4:

RACTERISTICS:

7 amino acids

no acid

SS: single

linear

E: peptide

URCE:

GenBank

85026

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lication US/09213392

505

ATION:

Bandman, Olga

Goli, Surya K.

ENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN

NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/213,392

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/083,661

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0128 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 87 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1085026

US-09-213-392-4

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US-09-083-661-4

Sequence 4: Application US/09083661

Patent No. 5955283

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

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; Sequence 3, Application US/08725531
; Patent No. 5756310
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga

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RTGPEDDE 75
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; Sequence 262, Application US/09989722
; Patent No. US2002007267A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferriara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989, 722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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100.0%; Score 461; DB 9; Length 89;
arity 100.0%; Pred.No. 5.8e-48;
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enazi, Avi J.
er, Kevin P.
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ber, Hanspeter
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ier, Mary A.
James
ni, Nicholas F.
Margaret Ann
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as, Daniel
anabe, Colin K.
liams, P. Mickey
i, William I.
ig, Zemin

ION: Secreted and Transmembrane Polypeptides and Nucleic
ION: Acids Encoding the Same
P2730PIC82

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; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nu
; FILE REFERENCE: P2730P1C56
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PRIOR FILING DATE: 1998-07-09

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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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arity 100.0%; Pred. No. 5.8e-48;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

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er, Kevin P.
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ritsen, Mary E.
dard, Audrey
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maldi, J. Christopher
ney, Austin L.
avin, Ivar J.
ier, Mary A.
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, Margaret Ann
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as, Daniel
anabe, Colin K.
liams, P. Mickey
d, William I.
ng, Zemin

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P2730PIC57

ION: Acids Encoding the Same
P2730PIC57

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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botstein, David
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; APPLICANT: Williams, P. Mickey
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; APPLICANT: Zhang, Zemin
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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100.0%; Score 461; DB 10; Length 89;
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US-09-990-456-262
; Sequence 262, Application US/09990456
; Patent No. US2002013790A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nu
; FILE REFERENCE: P2730PIC22
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; PRIOR APPLICATION NUMBER: 60/049787
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ker, Kevin P.
stein, David
snovers, Luc
ton, Dan L.
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imaidi, J. Christopher
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100.0%; Score 461; DB 10; Length 89;
 arity 100.0%; Pred. No. 5.8e-48;

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 ; Patent No. US20020160384A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nu
 ; TITLE OF INVENTION: Acids Encoding the Same
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 ; CURRENT APPLICATION NUMBER: US/09/992,598
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Query Match 100.0%; Score 461; DB 10; Length 89;
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idard, Audrey
owski, Paul J.
malidi, J. Christopher
ney, Austin L.
avin, Ivar J.
ier, Mary A.
i, James
ni, Nicholas F.
Margaret Ann
wart, Timothy A.
as, Daniel
anabe, Colin K.
liams, P. Mickey
d, William I.
ng, Zemin

TION: Secreted and Transmembrane Polypeptides and Nucleic
TION: Acids Encoding the Same

P2730PIC66

TION NUMBER: US/09/989,293A

DATE: 2001-11-20

ON NUMBER: 60/049787

TE: 1997-06-16

ON NUMBER: 60/062250

TE: 1997-10-17

ON NUMBER: 60/065186

TE: 1997-11-12

ON NUMBER: 60/065311

TE: 1997-11-13

ON NUMBER: 60/066770

TE: 1997-11-24

ON NUMBER: 60/075945

TE: 1998-02-25

ON NUMBER: 60/078910

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ON NUMBER: 60/083322

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TE: 1998-06-04

ON NUMBER: 60/088033

TE: 1998-06-04

ON NUMBER: 60/088326

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 ATE: 1998-07-07
 ION NUMBER: 60/092182
 ATE: 1998-07-09

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 Identity 100.0%; Pred. No. 5,8e-48;
 Conservative 0; Mismatches 0; Indels 0; Caps 0;

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KSSQKQHSVPPEKAIPITPGSATTC 89
 KSSQKQHSVPPEKAIPITPGSATTC 89

Application US/09989735
 US20020193299A1
 ION:
 tenazi, Avi J.
 cer, Kevin P.

APPLICANT: Botstein, David
 APPLICANT: Deenoyers, Luc
 APPLICANT: Eaten, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and N
 TITLE OF INVENTION: Acids Encoding the Same
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7	PRIOR FILING DATE: 1998-07-09	

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Job time : 32 secs

GenCore version 5.1.6
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in search, using sw model

uary 6, 2004, 16:01:30 ; Search time 21 Seconds
(without alignments)
407.572 Million cell updates/sec

-10-063-557-50

1 MERVTLALLLAGLTALEAN.....HSPVPEKAIPLITPGSATTC 89

OSUM62
pop 10.0 , Gapext 0.5

3308 seqs, 96168682 residues

is satisfying chosen parameters: 283308

3th: 0

3th: 2000000000

inimum Match 0%

aximum Match 100%

isting first 45 summaries

IR 76:*

Pir1:*

Pir2:*

Pir3:*

Pir4:*

the number of results predicted by chance to have a
c than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

seq	ch	Length	DB	ID	Description
1.6	87	2	I59391		transmembrane prot
1.4	88	2	S61552		mammary tumor prot
1.5	87	2	A55571		chloride conductan
1.4	92	2	A40533		CAMP-dependent pro
1.9	58	2	D46435		Na+/K+-exchanging
1.5	53	2	A46435		Na+/K+-exchanging
1.4	58	2	B46435		Na+/K+-exchanging
1.9	58	2	C46435		Na+/K+-exchanging
1.6	160	1	A61088		plastoquinol-plast
1.4	529	2	F69989		conserved hypothet
1.0	150	2	AH0371		probable membrane
1.6	135	2	A05009		hypothetical prote
1.4	359	2	A72004		chorismate synthas
1.4	339	2	B86620		chorismate synthas
1.4	523	2	A38101		potassium channel
1.3	446	2	B90463		potassium channel
1.9	525	2	A43531		potassium channel
1.8	309	2	AC1597		probable transport
1.8	309	2	AI1325		probable transport
1.8	511	2	A46020		potassium channel
1.8	511	2	S07095		potassium channel
1.8	585	2	A39395		delayed rectifier
1.8	620	2	A70525		hypothetical prote
1.7	468	2	C96818		hypothetical prote
1.6	239	2	A38111		transcription regu
1.6	679	2	A42073		potassium channel
1.6	769	2	I56546		Shaw type potassi
1.6	910	2	F81974		leucine-tRNA ligas
1.4	381	2	AB2907		GGDEF family prote

30 62 13.4 393 2 B97682 ggdef fami
31 62 13.4 589 2 T43295 uracil tra
32 62 13.4 777 2 S30271 pyocin AP4
33 61.5 13.3 342 2 S75086 iron-stres
34 61.5 13.3 433 2 H86597 flagellum-
35 61.5 13.3 433 2 B72025 flagellum-
36 61.5 13.3 433 2 AB1513 virulence
37 61.5 13.3 445 2 AD0962 DsdX perme
38 61.5 13.3 1499 2 AC2555 hypothetic
39 61 13.2 268 2 C87295 conserved
40 61 13.2 355 2 T51137 major hist
41 61 13.2 461 2 B90984 O antigen
42 61 13.2 463 2 A75151 damage-ind
43 61 13.2 463 2 G71191 probable DN
44 61 13.2 463 2 E85829 O antigen
45 61 13.2 520 2 D84471 O antigen
probable me

ALIGNMENTS

RESULT 1
I59391
transmembrane protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov
C/Accession: I59391
R/Attali, B.; Latter, H.; Rachamim, N.; Garty, H.
Proc. Natl. Acad. Sci. U.S.A. 92, 6092-6096, 1995
A/Title: A corticosteroid-induced gene expressing an 'IsK-like' K+ cha
A/Reference number: I59391; MUID:95320221; PMID:7597086
A/Accession: I59391
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-87 <RES>
A/Cross-references: GB:L41254; NID:G951422; PIDN:AAA74691.1; PID:G9514
C/Genetics:
A/Gene: 3D CHIF

Query Match 55.6%; Score 256.5; DB 2; Length 87;
Best Local Similarity 61.5%; Pred. No. 2.8e-21;
Matches 56; Conservative 11; Mismatches 17; Indels 7; G

QY 1 MERVTLA-LLLLAGLTALEANDPFANKDPFYVDWKNLQSLGICGSLAIAGTAA
Db 1 MEGITCAFLVLAGLPVLEANGP-VKGGPFYVDWESLQLGMPFGLLCIAGTAM
QY 60 KCKYKSSQKHSP--VPEKAIPLITPGSAT 88
Db 60 KCK---CRRHNPSSLPEKVTPLITPGSAST 87

RESULT 2
S61552
mammary tumor protein mat8 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-Nov
C/Accession: S61552; I48648
R/Morrison, B.W.; Leder, P.
Oncogene 9, 3417-3426, 1994
A/Title: neu and ras initiate murine mammary tumors that share genetic
A/Reference number: I48271; MUID:95060797; PMID:7970700
A/Accession: S61552
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-88 <MOR>
A/Cross-references: EMBL:X93038; NID:G1085067; PIDN:CAA63606.1; PID:gi
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F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-88/Product: mammary tumor protein mat8 #status predicted <MAT>
Query Match 52.4%; Score 241.5; DB 2; Length 88;

Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 19-AJ
C:Accession: D46435; S31525
R:Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Fox,
J. Cell Biol. 121, 579-586, 1993
A>Title: Molecular cloning and immunological characterization of the
A:Reference number: A46435; MUID:93252993; PMID:8387529
A:Accession: D46435
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-58 <MER>
A:Cross-references: EMBL:X70059; NID:g936; PIDN:CAA49663.1; PID:g9397
A>Note: The authors translated the codon TTC for residue 25 as Pro
C:Keywords: hydrolase; transmembrane protein

Query Match 20.9%; Score 96.5; DB 2; Length 58;
Best Local Similarity 34.6%; Pred. No. 0.00093;
Matches 18; Conservative 14; Mismatches 19; Indels 1;

QY 27 DDPPFYDNKLQSLGICGLLIAAGTAAVLGSCKYKSQKHSPVPEKAI 78
:|||||::: |||||::: |||||::: |||||:::
Db 8 EDPPFYDYEVRNGGLIPALAFIVGLVIILSKRFRC-GAKKRHQIPEDDL 51

RESULT 6
A46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - sheep (fragment)
N:A/Alternate names: sodium pump gamma chain; sodium/potassium-depender
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 22-Nov-1993 #sequence_revision 05-Dec-1998 #text_change 19-AJ
C:Accession: A46435; S31524; A27383
R:Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Fox,
J. Cell Biol. 121, 579-586, 1993
A>Title: Molecular cloning and immunological characterization of the
A:Reference number: A46435; MUID:93252993; PMID:8387529
A:Accession: A46435
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 6-53 <MER>
A:Experimental source: kidney
A>Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:131232, NCBIPI:13
R:Mercer, R.W.
submitted to the EMBL Data Library, December 1992
A>Description: Cloning and sequencing of gamma subunit of sodium pota
A:Reference number: S31522
A:Accession: S31524
A:Molecule type: mRNA
A:Residues: 6-19,'F',21-53 <MEW>
A:Cross-references: EMBL:X70061; NID:g1255; PIDN:CAA49665.1; PID:g125
R:Collins, J.H.; Leszyk, J.
Biochemistry 26, 8665-8668, 1987
A>Title: The "gamma-subunit" of Na,K-ATPase: a small, amphiphilic pro
A:Reference number: A27383; MUID:88163544; PMID:2831947
A:Accession: A27383
A:Molecule type: protein
A:Residues: 1-19,'F',21-33 <COL>
C:Complex: heterotrimer; alpha, beta, and gamma chain
C:Keywords: heterotrimer; hydrolase; transmembrane protein

Query Match 20.5%; Score 94.5; DB 2; Length 53;
Best Local Similarity 34.6%; Pred. No. 0.0014;
Matches 18; Conservative 14; Mismatches 19; Indels 1;

QY 27 DDPPFYDNKLQSLGICGLLIAAGTAAVLGSCKYKSQKHSPVPEKAI 78
:|||||::: |||||::: |||||::: |||||:::
Db 3 EDPPFYDYEVRNGGLIPALAFIVGLVIILSKRFRC-GAKKKHQIPEDDL 53

RESULT 7
A46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - rat

norvegicus (Norway rat)
 #sequence_revision 03-Feb-1994 #text_change 19-Apr-2002
 5; S31523
 emesederfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
 579-586, 1993
 cloning and immunological characterization of the gamma polypeptide,
 A46435; MUID:93252993; PMID:8387529
 5
 ary
 RNA
 MER>
 : EMBL:X70062; NID:g56299; PIDN:CAA49666.1; PID:g56300
 s translated the codon TTC for residue 25 as Pro
 ase; transmembrane protein
 16.4%; Score 75.5; DB 2; Length 58;
 arity 34.7%; Pred. No. 0.2;
 conservative 12; Mismatches 19; Indels 1; Gaps 1;
 YYDWKNLQSLGCGLLAAGIAAVALSGCKYKSKQKHSPVPE 75
 EYDVTVRKGLIFAGLAFVVGLLILSKRFRCCGS-KKRRQVNE 55
 5
 ATPase (EC 3.6.3.9) gamma chain - mouse
 culus (house mouse)
 #sequence_revision 03-Feb-1994 #text_change 19-Apr-2002
 5; S31522
 emesederfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
 579-586, 1993
 cloning and immunological characterization of the gamma polypeptide,
 A46435; MUID:93252993; PMID:8387529
 5
 ary
 RNA
 MER>
 : EMBL:X70060; NID:g51111; PIDN:CAA49664.1; PID:g51112
 s translated the codon TTC for residue 25 as Pro
 ase; transmembrane protein
 15.9%; Score 73.5; DB 2; Length 58;
 arity 32.7%; Pred. No. 0.33; Indels 1; Gaps 1;
 conservative 12; Mismatches 20; Indels 1; Gaps 1;
 YYDWKNLQSLGCGLLAAGIAAVALSGCKYKSKQKHSPVPE 75
 EYDVTVRKGLIFAGLAFVVGLLILSKRFRCCGS-KKRRQVNE 55
 55
 ocyanin reductase (EC 1.10.99.1) 17K protein - Synechocystis sp. (stra
 cytochrome b6-f complex chain IV; plastoquinol-plastocyanin reductase
 cystis sp.
 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
 8; S76298; S15474
 57, 336-342, 1992
 ion of insertion mutants of Synechocystis sp. PCC 6803: evidence for a
 A61088; MUID:92272582; PMID:11590707
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 NA
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 : EMBL:X58522; NID:947376; PIDN:CAA41412.1; PID:g47377
 S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 6, 1996
 analysis of the genome of the unicellular cyanobacterium Synechocystis
 : S74322; MUID:97061201; PMID:8905231

A:Accession: S76298
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-160 <KAN>
 A:Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAAL
 A:Note: the nucleotide sequence was submitted to the EMBL Data Librar
 C:Genetics:
 A:Gene: petD
 C:Superfamily: plastoquinol-plastocyanin reductase 17K protein; plast
 C:Keywords: oxidoreductase; photosynthesis; thylakoid
 F:24-144/Domain: plastoquinol-plastocyanin reductase 17K protein homo
 Query Match 15.6%; Score 72; DB 1; Length 160;
 Best Local Similarity 37.7%; Pred. No. 1.4;
 Matches 23; Conservative 9; Mismatches 21; Indels 8;
 QY 7 ALLLAGTAL-----EANDPFANKDD--PFYYDWKNLQSLGCGLLAAGI
 Db 47 ALGIAGLAILDPAIMIGEPADFFATPEILPEWVLYPTFQILRLPNKLLGIAGW
 QY 59 G 59
 Db 107 G 107
 RESULT 10
 F69989
 conserved hypothetical protein ytcJ - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun
 C:Accession: F69989
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; J
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.;
 A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; C
 tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hos
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapi
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.;
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.;
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; S
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; To
 I.; Winers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Ye
 A:Authors: Yoshikawa, H.F.; Zunshtein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium E
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: F69989
 A:Status: preliminary; nucleic acid sequence not shown; translation no
 A:Molecule type: DNA
 A:Residues: 1-529 <KUN>
 A:Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB1493
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ytcJ
 Query Match 15.4%; Score 71; DB 2; Length 529;
 Best Local Similarity 30.4%; Pred. No. 6.2;
 Matches 31; Conservative 9; Mismatches 24; Indels 38; G
 QY 16 ALEANDPFANKDDPFYYD-----WKNLQSLGCGG-----LL
 Db 381 ALDLPQHFVASFDFWVDRIGKDRMTAFATKTLISKGLCGAGSDAPIEPVDPDL
 QY 53 IAAVLGCKVKSKQKHSP-----VP-EKAIPLTIPGSA 86
 Db 440 -SAVLR-----KSSHEQNGFSYNESECLPVYEAIKLYTEGSA 475
 RESULT 11
 AH0371
 Probable membrane protein YPO3057 [imported] - Yersinia pestis (strain
 C:Species: Yersinia pestis

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001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
71
ren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
l.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
d, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
127; 2001
# sequence of Yersinia pestis, the causative agent of plague.
=: AB0001; MUID:21470413; PMID:11586360
171
nary
DNA
) <KUR>
15 : GB:AL530842; PIDN:CAC92299.1; PID:g15981010; GSPDB:GN00175

'poetical protein ytwI
    15.0%; Score 69; DB 2; Length 150;
    larity 30.2%; Pred.No. 2.8;
    Conservative 14; Mismatches 32; Indels 14; Gaps 4;

ALLLAGLTALEANDPFANKDPFYDWKNQLSLGICGLLAIAGI-AAVLGGCK 62
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AIIILLAIIRITPLNS-----FFPW--VEKYLTIGVILITGWAPIASG--K 72
SQQKHSPVPKEKAIPITPGSAT 88
|::|| :::|| :::|| :::||
SEVLHGFQWVKLSILAIVGVAVS 98

ein 135 - liverwort (Marchantia polymorpha) chloroplast
plast Marchantia polymorpha
87 #sequence_revision 05-Jun-1987 #text_change 08-Oct-1993
71: AO5009
okuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T.
e and Organization of Marchantia polymorpha chloroplast genome. II. Gen
x: SO1567; MUID:89068686; PMID:2974085
71
DNA
<DNE>
s: EMLX:XO4465; NID:g11640; PIDN:CAA28060.1; PID:g453590
zawaz, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
74; 1986
ast gene organization deduced from complete sequence of liverwort March
x: A38014
ation; Gene organization, sites, features
last
poetical protein 135
oplastr
    14.6%; Score 67.5; DB 2; Length 135;
    larity 32.6%; Pred.No. 3.7;
    Conservative 11; Mismatches 13; Indels 7; Gaps 2;

AG---LTALEANDPFANKDPFYDWKNQLSLGICGLLIAIAG 52
|::|| :::|| :::|| :::|| :::|| :::|| :::|| :::||
IGLFYALKLRFPYSRDYDFE----SCIGLLCGIIFFG 56

se CP0815 [imported] - Chlamydomonadales (strains CWLO29 and AR3
dophila pneumoniae, Chlamydia pneumoniae
99 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
04: D81536
chell,W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
385-389, 1999
ive genomes of Chlamydia pneumoniae and C. trachomatis.
```

[illegible]

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.n search, using sw model

uary 6, 2004, 16:00:10 ; Search time 11 Seconds
(without alignments)
380.489 Million cell updates/sec

10-063-557-50

ERTVTLALLLGLTALAN.....HSPVPEKAIPITPGSATTC 89

SUM62

op 10.0 , Gapext 0.5

'863 seqs, 47026705 residues

s satisfying chosen parameters: 127863

th: 0

th: 2000000000

nimum Match 0%

ximum Match 100%

string first 45 summaries

issProt_41:*

the number of results predicted by chance to have a
than or equal to the score of the result being printed,
d by analysis of the total score distribution.

SUMMARIES

Ch	Length	DB	ID	Description
16	89	1	FXV4 HUMAN	P59646 homo sapien
10	88	1	FXV4 MOUSE	Q9d2w0 mus musculus
6	87	1	FXV4 RAT	Q63113 rattus norv
4	88	1	FXV3 MOUSE	Q61835 mus musculus
9	88	1	FXV3 RAT	P59645 rattus norv
0	88	1	FXV3 PIG	Q97797 sus scrofa
5	87	1	FXV3 HUMAN	Q14802 homo sapien
0	92	1	PLM HUMAN	Q00168 homo sapien
4	92	1	PLM CANFA	P56513 canis famil
0	94	1	FXV6 RAT	Q91xv6 rattus norv
8	94	1	FXV6 MOUSE	Q9d164 mus musculus
1	92	1	PLM MOUSE	Q92239 mus musculus
5	92	1	PLM RAT	Q08589 rattus norv
4	95	1	FXV6 HUMAN	Q9hq03 homo sapien
9	58	1	ATNG BOVIN	Q04645 bos taurus
7	53	1	ATNG SHEEP	Q04680 ovis aries
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3	80	1	FXV7 HUMAN	P58549 homo sapien
4	80	1	FXV7 MOUSE	P59648 mus musculus
0	66	1	ATNG HUMAN	P54710 homo sapien
0	80	1	FXV7 RAT	P59649 rattus norv
9	66	1	ATNG RAT	Q04679 rattus norv
9	70	1	ATNG MOUSE	Q04646 mus musculus
4	93	1	FXV8 HUMAN	P58550 homo sapien
6	160	1	PETD SYN3	P27589 synchocyst
4	61	1	ATNG XENLA	Q13001 xenopus lae
2	184	1	FXV5 MOUSE	P97808 mus musculus
6	135	1	YC66 MARPO	Q32616 marchantia
5	330	1	AROC SULFO	Q96y94 sulfolobus
4	359	1	AROC CHLPN	Q926m2 chlamydia p
4	523	1	CIK3 HUMAN	P22001 homo sapien
9	525	1	CIK3 RAT	P15384 rattus norv

34	63.5	13.8	511	1	KNC1 HUMAN	P48547 homo
35	63.5	13.8	511	1	KNC1 MOUSE	P15388 mus
36	63.5	13.8	585	1	KNC1 RAT	P25122 ratt
37	62.5	13.6	299	1	COMQ BACSU	P33690 baci
38	62.5	13.6	769	1	KNC3 MOUSE	O63959 mus
39	62.5	13.6	910	1	SYL NEIMA	Q9jw39 neis
40	62.5	13.6	1048	1	SILA SALTY	Q9zhc9 salm
41	62	13.4	581	1	FUR4 SCHPO	Q10279 schi
42	61.5	13.3	342	1	ISIA SYN3	O55274 syne
43	61.5	13.3	524	1	P60 LISIV	Q01837 list
44	60.5	13.1	638	1	KNC2 RAT	P22462 ratt
45	60.5	13.1	728	1	PURL CANJE	Q9pny0 camp

ALIGNMENTS

RESULT 1
FXV4 HUMAN STANDARD; PRT; 89 AA.
AC P59646;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE FXVD domain-containing ion transport regulator 4 precursor.
GN FXVD4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RX MEDLINE-20408885; PubMed-10950925;
RA Sweadner K.J., Rael E.;
RT "The FXVD gene family of small ion transport regulators or channe
RT cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
CC -|- SURCELLULAR LOCATION: Type I membrane protein (Potential).
CC -|- SIMILARITY: Belongs to the FXVD family.
CC This SWISS-PROT entry is copyright. It is produced through a coll:
CC between the Swiss Institute of Bioinformatics and the EMBL Out:
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CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: A18299357 -; NOT ANNOTATED_CDS.
DR Genew; HGNC:4028; FXVD4.
DR PROSITE: P801310; FXVD; 1.
KW Transmembrane; Signal; Ionic channel; Ion transport.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 89 FXVD DOMAIN-CONTAINING ION TRANSPORT
FT REGULATOR 4.
FT DOMAIN 21 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 59 POTENTIAL.
FT DOMAIN 60 89 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 89 AA; 9373 MW; B595EF99A4949B4 CRC64;
Query Match 97.6%; Score 450; DB 1; Length 89;
Best Local Similarity 97.8%; Pred No. 8.8e-41;
Matches 87; Conservative 1; Mismatches 1; Indels 0; G:
QY 1 MERVTLALLLGLTALANPPFANKDDPFYVDWKNLQSLGICGGLLAIAAGAAV
Db 1 MERVTLALLLGLTALANPPFANKDDPFYVDWKNLQSLGICGGLLAIAAGAAV
QY 61 CKYKSSQKHSPVPEKAIPITPGSATTC 89

|||||
KSSQKQHSVPPEKAIPITPGSATTC 89

STANDARD; PRT; 89 AA.

(Rel. 41, Created)

(Rel. 41, Last sequence update)

(Rel. 41, Last annotation update)

containing ion transport regulator 4 precursor (Channel
tor) (CHIP).

(Mouse).

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Theria; Rodentia; Sciurognathi; Muridae; Mus.
0090;

M N.A.

VJ;

ence of mouse CHIP (FXVD4).";

AR-2001) to the EMBL/GenBank/DBJ databases.

M N.A.
/6J; TISSUE=Kidney;
5660; PubMed=11217851;

Inagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
zawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
azaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
atsuda H.A., Ashburner M., Batalov S., Casavant T.,
W., Gasterland T., Gissi C., King B., Kochiwa H.,
wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
ido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
felli D., Bojunga N., Carninci P., de Bonaldo M.F.,
J.F., Bult C., Fletcher C., Fujita M., Gariboldi M.,
rhill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
rchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
ato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
oyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
S., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
Y.;
annotation of a full-length mouse cDNA collection.";
85-690(2001).
LAR LOCATION: Type I membrane protein (Potential).
TY: Belongs to the FXVD family.

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-profit institutions as long as its content is in no way
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mail to license@isb-sib.ch).

29; AAK51508.1; -

28; BAB31372.1; -

9005; FXVD4

R000272; ATP1G1_PLM_MAT8.

8; ATP1G1_PLM_MAT8; 1.

1310; FXVD; 1.

e; Signal; Ionic channel; Ion transport.

1 20

21 88

FXVD DOMAIN-CONTAINING ION TRANSPORT

REGULATOR 4.

21 38

EXTRACELLULAR (POTENTIAL).

39 59

POTENTIAL.

60 88

CYTOPLASMIC (POTENTIAL).

8 AA; 9269 MW; 7EB0140941CFE926 CRC64;

Query Match 60.0%; Score 276.5; DB 1; Length 88;
Best Local Similarity 66.7%; Pred. No. 1.7e-22;
Matches 60; Conservative 8; Mismatches 19; Indels 3;

QY 1 MERVTLA-LLLLAGLTALANDPFAKDDPFYDWNKQLSLGGLGGLAAGI?
Db 1 MEEITCAFLLLLAGLPALEASDP-VDKDSPFYDWSLQGLGGLIFGGLLCIAGI?
QY 60 KCKYKSKQKQHSVPPEKAIPITPGSATTC 89
Db 60 KCKRRTHKP-SSLPGKATPLIIPGSANTC 88

RESULT 3

FXV4 RAT

ID_FXV4 RAT

AC Q63113; STANDARD; PRT; 87 AA.

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE FXVD domain-containing ion transport regulator 4 precursor (Char

DE inducing factor) (CHIP) (Corticosteroid-induced protein).

GN FXVD4.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra

ON NCBI_TaxID=10116;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=Mistar; TISSUE=Colon;

RX MEDLINE=95320221; PubMed=7597086;

RA Attali B., Latter H., Rachamim N., Garty H.;

RT "A corticosteroid-induced gene expressing an 'Isk-like' K+ chanr

activity in Xenopus oocytes";

RL Proc. Natl. Acad. Sci. U.S.A. 92:6092-6096(1995).

RN [2]

TISSUE SPECIFICITY.

RX MEDLINE=97000648; PubMed=8843704;

RA Capurro C., Coutry N., Bonvalet J.-P., Escoubet B., Garty H.,

Farman N.;

RT "Cellular localization and regulation of CHIP in kidney and colic

Am. J. Physiol. 271:C753-C762(1996).

CC -1- FUNCTION: Induces a potassium channel when expressed in xenc

oocytes.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: Selectively present in the distal parts

nephron (medullary and papillary collecting ducts and end pc

of cortical collecting tubule) and in the epithelial cells c

distal colon. No expression is found in renal proximal tubul

loop of henle and distal tubule, proximal colon, small intes

lung, choroid plexus, salivary glands, or brain.

CC -1- INDUCTION: By corticosteroids.

CC -1- SIMILARITY: Belongs to the FXVD family.

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CC -----

DR EMBL; L41254; AAA74691.1; -

DR PIR; I59391; I59391.

DR InterPro; IPR030272; ATP1G1_PLM_MAT8.

DR Pfam; PF02638; ATP1G1_PLM_MAT8; 1.

DR PROSITE; PS01310; FXVD; 1.

KW Transmembrane; Signal; Ionic channel; Ion transport.

FT SIGNAL 1 20

POTENTIAL.

FT CHAIN 21 87

FXVD DOMAIN-CONTAINING ION TRANSPOR

REGULATOR 4.

FT DOMAIN 21 38

EXTRACELLULAR (POTENTIAL).

39 59 POTENTIAL.
60 87 CYTOPLASMIC (POTENTIAL).
AA: 9084 MW; 5D0DE1FC6B1BCA CRC64;
arity 55.6%; Score 256.5; DB 1; Length 87;
conservative 11; Mismatches 17; Indels 7; Gaps 4;
TLA-LLLAGLTALEANDPPANKDPPFYDWKNLQSLGCGGLAIAAGIAVLGS 59
ICAFLLVLAGLPVLEANGP-VDRKSPFYDWESLQGLGMIFGGLICIAIAVALSG 59
KSQKQHP--VPEKAIPITPGSATT 88
--CRNHTPSLPEKVTPLITPGSAST 87
STANDARD; PRT; 88 AA.
Rel. 36, Created)
Rel. 36, Last sequence update)
Rel. 42, Last annotation update)
containing ion transport regulator 3 precursor (Chloride
inducer protein Mat-8) (Mammary tumor 8 kDa protein)
1-like).
OR PLML.
(Mouse).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
390;
N.A.
TISSUE=Breast;
797; PubMed=7970700;
Leder P.;
initiate murine mammary tumors that share genetic
ally absent in c-myc and int-2-initiated tumors.";
17-3426(1994).
N.A.
tumor;
257; PubMed=12477932;
G., Feingold E.A., Grouse L.H., Derge J.G.,
Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Tuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Ewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Con E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
idan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Touchman J.W., Green E.D., Dickson M.C.,
Grimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schein J.E., Jones S.J.M., Marra M.A.,
ad initial analysis of more than 15,000 full-length
se cDNA sequences.";
Cad. Sci. U.S.A. 99:16899-16903(2002).
184; PubMed=7836447;
Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,
el phospholeman-like protein expressed in human breast
es a chloride conductance in Xenopus oocytes.";
. 270:2176-2182(1995).
Induces a hyperpolarization-activated chloride current

when expressed in xenopus oocytes. May be a modulator capable
activating endogenous oocyte channels.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: Expressed in a subset of murine breast tu
-!- MISCELLANEOUS: Marker of a cell type preferentially transform
neu or ras oncogene protein.
-!- SIMILARITY: Belongs to the FXD family.
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entitles requires a license agreement (See <http://www.isb-sib.ch/>
or send an email to license@isb-sib.ch).
EMBL; X93038; CAA63606.1; --
EMBL; BC002039; AAH02039.1; --
PIR; S61552; S61552.
MGD; MGI:107497; Fxyd3.
InterPro; IPR00272; ATP1G1_PLM_MAT8.
Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
PROSITE; PS01313; FXYD; 1.
Transmembrane; Signal; Ionic channel; Chloride channel; Chloride;
Ion transport.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 88 FXYD DOMAIN-CONTAINING ION TRANSPORT
REGULATOR 3.
FT DOMAIN 21 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 59 POTENTIAL.
FT DOMAIN 60 88 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 88 AA; 9526 MW; 9CD61684B856E35D CRC64;
Query Match 52.4%; Score 241.5; DB 1; Length 88;
Best Local Similarity 57.8%; Pred. No. 8.5e-19;
Matches 52; Conservative 11; Mismatches 24; Indels 3; G
QY 1 MERVTLALL-LLAGLTALEANDPPANKDPPFYDWKNLQSLGCGGLAIAAGIAA
Db 1 MQEVLVSLVLAGLPVLEANGP-ENKNDPPFYDWYSLVRGGLICAGILCALGIIV
QY 60 KCKYKSSQKHSPVPEKAIPLITPGSATT 89
Db 60 KCKKFRQKP-SHRPGEGPLITPGSAHC 88
RESULT 5
FXY3 RAT
ID -FXY3 RAT STANDARD; PRT; 88 AA.
AC P59645;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE FXYD domain-containing ion transport regulator 3 precursor.
GN FXYD3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee N.H., Glodek A., Chandra I., Mason T.M., Quackenbush J.,
RA Kerlavage A.R., Adams M.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RX MEDLINE=20408885; PubMed=10950925;
RA Sweadner K.J., Rael E.;
RT "The FXYD gene family of small ion transport regulators or channe
cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
CC -!- FUNCTION: Induces a hyperpolarization-activated chloride curr
when expressed in xenopus oocytes. May be a modulator capable

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RC	SEQUENCE FROM N.A.
RP	TISSUE=Urinary bladder;
RX	MEDLINE=223825; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.
RA	Altshul R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schetz
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C
RA	Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mulliahy
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk
RA	Villalon D.K., Muzley D.M., Sadegzadeh F., Tan X., Gibbs P.A.

GN FXD1 OR PLM.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 (1)
 RN SEQUENCE FROM N.A.
 RP TISSUE=Heart;
 RC MEDLINE=97312702; PubMed=9169143;
 RX Chen L.-S.K., Lo C.F., Numann R., Cuddy M.;
 RT "Characterization of the human and rat phospholemman (PLM) cDNAs
 RT localization of the human PLM gene to chromosome 19q13.1.";
 RL Genomics 41:435-443 (1997).
 (2)
 RN SEQUENCE FROM N.A.
 RP SWEADNER K.J., Rael E.;
 RX MEDLINE=20408885; PubMed=10950925;
 RT "The FXD gene family of small ion transport regulators or channel
 RT cDNA sequence, protein signature sequence, and expression.";
 RL Genomics 68:41-56 (2000).
 (3)
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain, Lung, and Testis;
 RC MEDLINE=22386257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.I.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton C.M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carinci P., Prange C.
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F.
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk E.
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in xenopus oocytes. May have a functional role
 CC in muscle contraction.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Highest expression in skeletal muscle and
 CC heart. Moderate levels in brain, placenta, lung, liver, pancreas,
 CC uterus, bladder, prostate, small intestine and colon with mucosal
 CC lining. Very low levels in kidney, colon and small intestine
 CC without mucosa, prostate without endothelial lining, spleen,
 CC testis.
 CC -!- PTM: Major plasma membrane substrate for camp-dependent protein
 CC kinase (PK-A) and protein kinase C (PK-C) in several different
 CC tissues (By similarity). Phosphorylated in response to insulin
 CC adrenergic stimulation.
 CC -!- SIMILARITY: Belongs to the FXD family.

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 CC boration between the Swiss Institute of Bioinformatics and the EMBL out-
 CC put of the European Bioinformatics Institute. There are no restriction
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 CC the public domain and this statement is not removed. Usage by and for com-
 CC mercial entities requires a license agreement (See <http://www.isb-sib.ch/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; U72245; AAC51286.1; -;
 DR EMBL; BC032800; AAC51286.1; -;
 DR Genbank; HGNC:4025; FXD1.
 DR MIM; 602359; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.

54; F:chloride channel activity; TAS.
121; P:chloride transport; TAS.
336; P:muscle contraction; TAS.
R000272; ATP1G1.PLM MAT8.
8; ATP1G1.PLM MAT8; 1.
1310; FXVD; 1.
e; Phosphorylation; Signal; Ionic channel;
annel; Chloride; Ion transport.
1 20
21 92
21 35
21 35
36 56
57 92
83 83
88 89
3 3
5 5
2 AA; 10441 MW; 11602EFEAFEDBD8 CRC64;
28.0%; Score 129; DB 1; Length 92;
larity 41.3%; Pred. No. 6.5e-07;
Conservative 15; Mismatches 20; Indels 2; Gaps 1;
LEANDPEFANKDDPFYDKNLQSLGICGGLAIAAGIAVLGKCKYKSSQKOHSPV 73
AKAESP--KEHDPFTYDQSLQGGLVIAGILFILGILVLSRCRCRCKFNQOQTGE 72
76
75
STANDARD; PRT; 92 AA.
(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41; Last annotation update)
n precursor (FXVD domain-containing ion transport
avis (Dog).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Carnivora; Fissipedia; Canidae; Canis.
615.
M N M N A., AND SEQUENCE OF 21-92.
icular muscle:
0422; PubMed:1710217;
Scott B.T., Jones L.R.;
n and complete sequence determination of the major plasma
nstrate for CAMP-dependent protein kinase and protein
myocardium";
m. 266:11126-11130(1991).
: Induces a hyperpolarization-activated chloride current
ressed in xenopus oocytes. May have a functional role in
contraction.
LAR LOCATION: Type I membrane protein.
SPECIFICITY: Present in heart, esophagus, stomach, aorta,
muscle, smooth muscle, and liver but absent from brain
ey.
or plasma membrane substrate for camp-dependent protein
PK-A) and protein kinase C (PK-C) in several different
phosphorylated in response to insulin and adrenergic
ion (By similarity)
TY: Belongs to the FXVD family.
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3; BARG2242.1; -
9; AARG6613.1; -
300272; ARIPL1_PLM_MATS.
; ARIPL1_PLM_MATS_1.
310; FXID; 1.
; Signal; Ionic channel; Ion transport;
plicing.

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1	POTENTIAL.
17	FXID DOMAIN-CONTAINING ION TRANSPORT
18	REGULATOR 6.
94	EXTRACELLULAR (POTENTIAL).
	POTENTIAL.
18	CYTOPLASMIC (POTENTIAL).
35	Missing (in isoform 2).
57	/FTid=VSP001586.
94	N -> S (IN REF. 2).
20	
65	
AA:	1C0D35FA0C572451 CRC64:
	10388 MW:

27.0%; Score 124.5; DB 1; Length 94;
arity 37.5%; Pred. No. 2e-06;
onservative 15; Mismatches 37; Indels 2;

TLALLLAGLTALEANDPFANKDDPFYDWNKQLSLGICGGLLATAGIAAVALSGK 60
: ||| : | ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
LILCSLLAPVVLASAAEKEKEK-DPFYDYDQTLRIGGLVFAVVLSEVGILLILSR 59

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SSQKQHSPVPEKA--IPLITPGSA 86
      :|| : ||| :||| :|
FNQKPRAPGDEEAQVENLITTNAA 87
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STANDARD;                                PRT;      94 AA.
3; Q9CXD0;
Rel. 41, Created)
Rel. 41, Last sequence update)
Rel. 41, Last annotation update)
containing ion transport regulator 6 precursor (PLM)-like

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(Mouse).
 Insecta; Craniata; Vertebrata; Euteleostomi;
 Lacoza; Chordata; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 090;

N.A. (ISOFORM 1).
6; TISSUE=Cerebellum;
Ooba R., Kato K., Matsubara K.;
like ion channel gene expressed in the nervous system.";
3-1999) to the EMBL/GenBank/DBJ databases.

N.A. (ISOFORMS 1 AND 2).
60; TISSUE=Embryo;
660; PubMed=11217851;
nagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
ara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
awa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
zaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,
tsuda H.A., Ashburner M., Batalov S., Casavant T.,
Gaasterland T., Gissi C., King B., Kochiwa H.,
is S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
do T., Furuno M., Anon H., Bairdrell R., Barsh G.,
felli D., Bojunga N., Carninci P., de Bonaldo M.F.,
J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Maehama J., Mazzaralli J., Mombers P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seyta T., Shibata Y., Storch K.
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilmir
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RT

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=FVB/N; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;

KA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.I

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko I., Marxins V., Farmer A., Rubin C.M., Hoeg I.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F.
PA Richards S., Worley K.C., Hulett C., Gonzalez A.M., Gonzalez M., Hulett C.

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk E.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -I- ALTERNATIVE PRODUCTS:

```
CC      -!- ALTERNATIVE PRODUCTS;
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
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CC      IsId=Q9D164-1; Sequence=Displayed;
CC      Name=2;
CC      IsId=Q9D164-2; Sequence=VSP_001505;
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CC      Isoid=Q9D164-2; Sequence=VSP_001585;
CC
CC      -!- SIMILARITY: Belongs to the FYD family.
CC      -----

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CC entities requires a license agreement (See <http://www.isb-sib.ch/> or send an email to license@isb-sib.ch).

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CC -----
DR EMEL; AB032010; BAB40451.2; -.
DR EMEL; AK003888; BAB23058.1; -.

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DR	EMBL	AK003666	BAB23058.1	-
DR	EMBL	AK018354	BAB31174.1	-
DR	EMBL	BC042579	AAH42579.1	-

DR EMBL; BC051127; AAH51127.1; -.
DR MGD; MGI:1890226; Fxyd6.
DR InterPro; IP000272: ATP1G1 PLM MAT8.

DR INTEIFIO; IFR000272; ATP1G1_PLM_MAT8.
DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR PROSITE; PS01310; FXD; 1.

KW Transmembrane; Signal; Ionic channel; Ion transport;
KW Alternative splicing.
ET SIGNAL 1 17 POTENTIAL.

FT	SIGNAL	1	17	POTENTIAL.
FT	CHAIN	18	94	FXD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 6.
FT				

FT	DOMAIN	18	34	EXTRACELLULAR (POTENTIAL),
FT <td>TRANSMEM</td> <td>35</td> <td>57</td> <td>POTENTIAL.</td>	TRANSMEM	35	57	POTENTIAL.
FT <td>DOMAIN</td> <td>58</td> <td>94</td> <td>CYTOPLASMIC (POTENTIAL)</td>	DOMAIN	58	94	CYTOPLASMIC (POTENTIAL)

FT	DOMAIN	58	94	CYTOPLASMIC (POTENTIAL).
FT	VARSPIC	20	20	Missing (in isoform 2).
FT				/FTid=VSP 001585.

SQ SEQUENCE 94 AA; 10374 MW; 02E22B0BE349CB51 CRC64;

Query Match	26.8%;	Score 123.5;	DB 1;	Length 94;
Best Local Similarity	37.5%;	Pred. No. 2.5e-06;		
Matches 33;	Conservative	15;	Mismatches 37;	Indels 3; G

CC	EMBL; AF091390; AAD11781.1; -	
CC	EMBL; AF089734; AAD11683.1; -	
DR	EMBL; AK002585; BAB2208.1; -	
DR	MGD; MGI:1889273; Fxyd1.	
DR	InterPro; IPR000272; ATP1G1_PLM_MATS.	
DR	Pfam; PF02038; ATP1G1_PLM_MATS; 1.	
DR	PROSITE; PS01310; FXYD_1	
KW	Transmembrane; Phosphorylation; Signal; Ionic channel;	
KW	Chloride channel; Chloride; Ion transport	
FT	SIGNAL	1 20
FT	CHAIN	21 92
FT	DOMAIN	21 35
FT	TRANSMEM	36 56
FT	DOMAIN	57 92
FT	MOD_RES	83 83
FT	MOD_RES	88 88
FT	SEQUENCE	92 AA, 10323 MW;
SQ	OBDB1DC83417P3AD CRC64;	
SQ	OBDB1DC83417P3AD CRC64;	

FT	92	PHOSPHOLEMAN.
CHAIN	21	EXTRACELLULAR (POTENTIAL).
DOMAIN	35	POTENTIAL.
TRANSMEM	56	CYTOPLASMIC (POTENTIAL).
FT DOMAIN	57	PHOSPHORYLATION (BY PKC AND PKA) (E
MOD_RES	83	SIMILARITY).
FT	88	PHOSPHORYLATION (BY PKA) (BY SIMILAR
MOD RES	88	PHOSPHORYLATION (BY PKA);
SEQUENCE	92 AA,	0DBD1DC8341F73AD CRC64;
FT	10323 MW;	
SQ		

TRANSMEM	36	56	POTENTIAL.
FT	57	92	CYTOPLASMIC (POTENTIAL).
FT DOMAIN	52	92	
FT MOD_RES	83	83	PHOSPHORYLATION (BY PKC AND PKA) (E
FT			SIMILARITY).
FT			
FT MOD_RES	88	88	PHOSPHORYLATION (BY PKA) (BY SIMILAR
FT			
FT SQ	92 AA	10323 MW;	0BDB1DC8341F3AD CRC64;

	83	CYCLOPHOSPHAMIC ACID POLYMERIZATION.
FT	87	PHOSPHORYLATION (BY PKC AND PKA) (E
MOD_RES	83	SIMILARITY).
FT	88	PHOSPHORYLATION (BY PKA) (BY SIMILAR
MOD_RES	88	ITY).
FT	92 AA	SEQUENCE - 92 AA; 10323 MW; OBD1DC8341F3AD CRC64;
SQ		

FT	MOD RES	88	88	PHOSPHORYLATION (BY PKA)	(BY SIMILARITY)
SQ	SEQUENCE	92 AA;	10323 MW;	08DB1DC83417F3AD	CRC64;

Score	23.18; Score	215.3; D5	1
Best Local Similarity	34.2; Pred.	No. 1.7e-05;	
Matches	25; Conservative	17; Mismatches	26; Indels
			5;

[illegible]

db 8 LALCVLLSMAAEAPQEP-----DPETYDHTLRIGGLTIAGILEFILGILLIS

QY	64	KSSQKQHSVPPEK	76
		: : : :	
DB	63	KFNOQORTGEPDE	75

Db 63 KFNQQRTGEPDE 75

PROFIT 13

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RESULTS IS
PLM_RAT
ID_PLM_RAT STANDARD; PRT; 92 AA.

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ID	PLM_RAT	STANDARD;	PRT;	92 AA.
AC	O08589;			
AD		15-JUL-1998 (Rel. 36, Created)		
AT		28-FEB-2003 (Rel. 41, Last sequence update)		
DT		28-FEB-2003 (Rel. 41, Last annotation update)		
DE		Phospholemman precursor (FX1D domain-containing ion transport regulator 1).		
DE		FX1D1 OR F1M.		
GN		Rattus norvegicus (Rat).		
OS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra		
OX		NCBI TaxID=10116;		
RN		[1] _RN		
RP		SEQUENCE FROM N.A.		
RC		TISSUE=Heart;		
RC		MEDLINE=97312702; PubMed=9169143;		
RR		Chen L.-S.K., Lo C.F., Numann R., Cuddy M.;		
RR		"Characterization of the human and rat phospholemman (PLM) cDNAs		
RT		localization of the human PLM gene to chromosome 19q13.1.";		
RT		Genomics 41:435-443(1997).		
RRL		[2]		

SEQUENCE FROM N.A.
MEDLINE=20408885; PubMed=10950925;

-1- FUNCTION: Induces a hyperpolarization-activated chloride current when expressed in xenopus oocytes. May have a fictional role

when exposed to xenopus oocytes, may have a functional role in muscle contraction.

```

CC CC SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -- PMW: Major plasma membrane substrate for camp-dependent prot
CC CC kinase (PK-A) and protein kinase C (pk-C) in several differe
CC CC tissues. Phosphorylated in response to insulin and adrenergi
CC CC stimulation (By similarity).
CC CC -- SIMILARITY: Belongs to the FXD family.
CC CC -----
CC CC This SWISS-PROT entry is converted. It is produced through a col

```

RC
ISSUE=Kidney;

1. **Исходные данные:**

10. 11. 2019. 14:00

09:53:14 2004

us-10-063-557-50.rspt

GenCore version 5.1.6
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main search, using sw model

January 6, 2004, 16:00:40 ; Search time 36 Seconds
(without alignments)
637.963 Million cell updates/sec

3-10-063-557-50

1
MERVTLALLLAGLTALEAN.....HSPVPEKAIPITPGSATTC 89

JOSUM62

ipop 10.0 , Gapext 0.5

10525 seqs, 258052604 residues

ts satisfying chosen parameters: 830525

lgth: 0

lgth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

PTREMBL_23:*

sp_archaea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mhc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rodent:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_rvirus:*

sp_bacteriopl:*

sp_archaeap:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

ery	tch	Length	DB	ID	Description
8.4	80	11	Q8BTD2	Q8BTD2 mus musculus	
8.2	178	4	Q8IWS1	Q8IWS1 homo sapien	
5.9	196	5	Q9GZE7	Q9GZE7 caenorhabdi	
5.8	1132	12	Q83861	Q83861 nilaparvata	
5.4	529	16	C34355	C34355 bacillus su	
5.0	150	16	Q8ZCB4	Q8ZCB4 yersinia pe	
5.0	157	16	Q8D0V1	Q8D0V1 yersinia pe	
4.9	339	10	Q9LUK8	Q9LUK8 arabidopsis	
4.9	340	10	Q94E19	Q94E19 arabidopsis	
4.9	456	16	Q9CL30	Q9CL30 pasteurella	
4.8	173	8	Q8HXR3	Q8HXR3 arcos sp. k	
4.6	664	4	O75485	O75485 homo sapien	
4.6	664	4	Q8WU17	Q8WU17 homo sapien	
4.4	241	16	Q9K3I3	Q9K3I3 streptomyce	
4.4	516	6	Q28656	Q28656 oryctolagus	
4.4	549	16	Q8E9W6	Q8E9W6 shewanella	

17	66	14.3	446	17	Q97UY7	su
18	65.5	14.2	546	4	Q86NJ9	hom
19	65.5	14.2	582	4	Q8N8P9	hom
20	65.5	14.2	1185	16	Q8EGS8	sh
21	65	14.1	327	10	Q9LVG3	ar
22	65	14.1	469	2	Q9XDX1	mag
23	65	14.1	760	13	Q90638	ga
24	64.5	14.0	155	11	Q9R126	mu
25	64.5	14.0	455	17	Q8TXS5	py
26	64.5	14.0	465	2	O86080	rho
27	64.5	14.0	550	12	Q9QEW9	me
28	64.5	14.0	550	12	Q9QEW7	me
29	64.5	14.0	725	5	Q8SY05	dro
30	64	13.9	315	10	Q9LS88	ar
31	64	13.9	667	5	Q9BJM1	tri
32	64	13.9	678	16	Q8R9G1	th
33	63.5	13.8	309	16	Q82A05	li
34	63.5	13.8	309	16	Q8YSP7	li
35	63.5	13.8	550	12	Q9QEW8	me
36	63.5	13.8	585	6	Q9XSJ8	can
37	63.5	13.8	620	16	O07239	my
38	63.5	13.8	882	10	Q8LSV5	or
39	63	13.7	468	10	Q9ZVA7	ar
40	63	13.7	655	2	Q8KWT9	str
41	63	13.7	655	16	Q8DUN3	st
42	63	13.7	825	12	Q993G5	ca
43	63	13.7	912	16	O8D4M3	vi
44	63	13.7	923	5	Q9N389	cae
45	63	13.7	1022	5	Q27779	sch

ALIGNMENTS

RESULT 1

ID	Q8BTD2	PRELIMINARY;	PRT;	80 AA.
AC	Q8BTD2;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	FXD domain-containing ion transport regulator 7.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Body;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotat			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK004113; BAC35067.1;			
SQ	SEQUENCE 80 AA; 8487 MW; 135CEB39C7A01CDC CRC64;			

Query Match	18.4%;	Score 85;	DB 11;	Length 80;
Best Local Similarity	29.5%;	Pred. NO. 0.04;		
Matches	23;	Conservative 14;	Mismatches 35;	Indels 6;
QY	11 LAGTALZANDPPFANKDPFYVDWKNLQSLGICGLLAIAGIAVLGKCK-YK			
Db	1 MATQTSTNVP--EETDPFYDYATVQTGNTLATIMFVLGIIILSKVKCKRK			
QY	70 HSPVPEKA---IPLITPG 84			
Db	59 ESPTCKSCKSELPSAPG 76			
RESULT 2				
Q8IWS1				

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PRELIMINARY; PRT; 178 AA.
(TREMBLrel. 23, Created)
(TREMBLrel. 23, Last sequence update)
(TREMBLrel. 23, Last annotation update)
as associated transmembrane protein 1.
; (Human).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Primates; Catarrhini; Hominidae; Homo.
606;
M N.A.
; Takao J., Das A., Cruz P.D. Jr., Ariizumi K.;
; Ion of genes for secreted and membrane-anchored proteins
ytes."
; CT-2002) to the EMBL/GenBank/DBJ databases.
; 82; AAO13166.1; -.
le.
.78 AA; 19313 MW; 8129COAD3A449584 CRC64;
.arity 18.2%; Score 84; DB 4; Length 178;
Conservative 7; Mismatches 15; Indels 6; Gaps 1;
A-----NKDPPFYDWNKQLSLGICGGLLAIAAGIAAVLSGKC 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
ALKPSGFHEDDSFFYDEHTLRKGLLVAALVITGITIILTSKC 166
PRELIMINARY; PRT; 196 AA.
(TREMBLrel. 16, Created)
(TREMBLrel. 16, Last sequence update)
(TREMBLrel. 23, Last annotation update)
.20.5 kDa protein.
is elegans.
Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Peloderinae; Caenorhabditis.
239;
M N.A.
.01 N2;
.9613; PubMed=9851916;
ence of the nematode C. elegans: a platform for
g biology. The C. elegans Sequencing Consortium."
2012-2018(1998).
M N.A.
.01 N2;
amsley P.;
e of C. elegans cosmid F49F1."
CT-1998) to the EMBL/GenBank/DBJ databases.
M N.A.
.01 N2;
;
ission."
UG-2001) to the EMBL/GenBank/DBJ databases.
156; AAF39970.1; -.
IF1.3; CE25894.
rotein.
.96 AA; 20528 MW; 41FA957F66B44399 CRC64;
arity 15.9%; Score 73.5; DB 5; Length 196;
Conservative 14; Mismatches 22; Indels 25; Gaps 5;
ALLLIA--GLTALEANDPFANKDPFYDWNKQLSLGII--CGGLL-AIAGIAAVLS 58
PRELIMINARY; PRT; 1132 AA.
Q83861;
ID Q83861 PRELIMINARY; PRT; 1132 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 130KD protein.
OS Nilaparvata lugens reovirus.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
CX NCBI_TaxID=33724;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IZUMO;
RX MEDLINE=96145144; PubMed=8558122;
RA Nakashima N., Koizumi M., Watanabe H., Hiroaki N.;
RT "Complete nucleotide sequence of the Nilaparvata lugens reovirus
RT putative member of the genus Fibivirus.";
RL J. Gen. Virol. 77:139-146(1996).
DR EMBL; D49696; BAA08545.1; -.
DR InterPro; IPR002877; FcSJ.
DR Pfam; PF01728; FcSJ; 1.
SQ SEQUENCE 1132 AA; 130041 MW; 6EBF5714B8EA0576 CRC64;
Query Match 15.8%; Score 73; DB 12; Length 1132;
Best Local Similarity 28.6%; Pred. No. 19;
Matches 22; Conservative 17; Mismatches 22; Indels 16;
QY 10 LLAGLTALANDPFANKDPFYDWNK-----LQSLGICGGLLAIAAGIAAVLSK
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
837 LVYGITSLDRLSLFAR--DPIFYQYSLHSLTKLNGTKIKADFIKIGISPIITS
Db
QY 65 SSQKQ-----HSPVPEK 76
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
891 NAQRYQLSNVHSDIMDK 907
Db
RESULT 5
Q34355
ID Q34355 PRELIMINARY; PRT; 529 AA.
AC Q34355;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE YTCJ.
GN YTCJ.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bror
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson E.
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.

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laser P., Goffeau A., Golightly E.J., Grandi G.,
 Guy B.-J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 ramana D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 Koetter P., Koningsstein G., Krogh S., Kumano M.,
 vidus A., Lardinois S., Lauber J., Lazarevic V.,
 apine A., Liu H., Masuda S., Mauel C., Medigue C.,
 ellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 hl T.M., Portelle D., Porwollik S., Prescott A.M.,
 Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 ivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 alan E., Schleich S., Schroeter R., Scoffone F.,
 Sekowska A., Seror S.J., Serrif P., Shin B.S., Solido B.,
 faconi E., Takagi T., Takahashi H., Takenaru K.,
 Chiyama S., Tanaka T., Terpstra P., Tognoni A.,
 chiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 mbat R., Wedler E., Wedler H., Weitzenegger T.,
 iput A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 genome sequence of the gram-positive bacterium *Bacillus*
 19-256(1997) .
 4 N.A.
 isawara N., Yoshikawa H., Danchin A.;
 20-1997) to the EMBL/GenBank/DBJ databases.
 20; AAC00311.1; -.
 3; CAB14933.1; -.
 3006680: Amidohydro.1.
 3; Amidohydro_1; 1.
 ceome.
 29 AA; 58476 MW; A582764A05C8AC12 CRC64;
 15.4%; Score 71; DB 16; Length 529;
 arity 30.4%; Pred.No.13;
 conservative 9; Mismatches 24; Indels 38; Gaps 6
 NDPFANKDDPPFYD-----WKNLQLSLGICGG-----LLATAG 52
 QPHFVASDPFWIDRLGDKRMKTAFAWKTLISKGLCAGSDAPIEPVDPLGIQ- 439
 TSGCKYKYSQKHSP-----VP-EKAIPLTIPGSA 86
 LR-----KSSHEQNGPSYNESECLPVYEAIKLYTEGSA 475
 RELIMINARY; PRT; 150 AA.
 TREMBLrel. 20, Created)
 TREMBLrel. 20, Last sequence update)
 TREMBLrel. 23, Last annotation update)
 rane protein.
 is.
 teobacteria; Gammaproteobacteria; Enterobacteriales;
 aceae; Yersinia.
 2;
 N.A.
 / Biovar Orientalis;
 413; PubMed=11586360;
 Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 , Sebahia M., James K.D., Churcher C., Mungall K.L.,
 ham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.M.,
 T., Cronin A., Davies R.M., Davis P., Dougan G.,
 Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 oule S., Oyston P.C.F., Quail M., Rutherford K.,
 Skelton J., Stevens K., Whitehead S., Barrall B.G.;
 nce of *Yersinia pestis*, the causative agent of plague."

Best Local Similarity 29.0%; Pred. No. 16;
Matches 20; Conservative 15; Mismatches 21; Indels 13;

QY 33 DMKNLQLSL-----ICGGLLAAGIAAVLSGCKKYKSG--KHSPF
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 270 DWVWLVLSALLEADTKLTITINLFVGAIALAGVAAYNNHKLKEASKVVTTETP

QY 80 LITPSAAT 88
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 330 LVSQNGTNT 338

RESULT 10
Q9CL30 PRELIMINARY; PRT; 456 AA.

ID Q9CL30 AC Q9CL30; DB Q9CL30; EMBL Q9CL30; GI Q9CL30; RefSeq Q9CL30;
DC Q9CL30; UniProt Q9CL30; TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PM1417.
GN PM1417.
GE DE
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurelia.
OX NCBI_TaxID=747;
[1] RN SEQUENCE FROM N.A.
RP STRAIN:Pm70;
RC MEDLINE=21145866; PubMed=11248100;
RX May B.J., Zhang Q., Li D.L., Paustian M.L., Whittam T.S., Kapur
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006178; AAK03501.1; -;
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00654; voltage_CLC; 1.
DR PRINTS; PROU762; CLCHANNEL.
DR Hypothetical protein; Complete proteome.
SK SEQUENCE 456 AA; 49349 MW; AA9C46DB68D4ED0A CRC64;
KW

Query Match 14.9%; Score 68.5; DB 16; Length 456;
Best Local Similarity 29.7%; Pred. No. 22;
Matches 22; Conservative 14; Mismatches 23; Indels 15;

QY 2 ERVTLLALLLAG--ITALANDPF-----ANKDDPPFYDWKNLQLSLGILC---G
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 211 ERRVLGLVLAAGFILVAIEGNNPFPQHGTSVPYLFLW--VSICGVWCVGFFG

QY 50 -IAG-AAVLSGCK 62
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 269 LVKGLAGLSPSKIR 282

RESULT 11
Q8HKR3 PRELIMINARY; PRT; 173 AA.

ID Q8HKR3 AC Q8HKR3; DB Q8HKR3; EMBL Q8HKR3; GI Q8HKR3; RefSeq Q8HKR3;
DC Q8HKR3; UniProt Q8HKR3; TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 6.
GN ND6.
GE DE
OS Arcos sp. KU-149.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Perciformes;
OC Gobiesocidae; Gobiesocidae; Arcos.
OX NCBI_TaxID=181474;
[1] RN SEQUENCE FROM N.A.
RP TISSUE=Muscle;
RC Miya M.;
RA Submitted (DSC-2001) to the EMBL/GenBank/DBI databases

[illegible]

Query Match 14.4%; Score 66.5; DB 16; Length 241;
Best Local Similarity 28.4%; Pred. No. 18;
Matches 27; Conservative 15; Mismatches 32; Indels 21; <

Query Match 14.4%; Score 66.5; DB 16; Length 241;
Best Local Similarity 28.4%; Pred. No. 18;
Matches 27; Conservative 15; Mismatches 32; Indels 21; <

XX
KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
PN WO200000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
XX
PR 11-DEC-1998; 98US-0112129.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI; 2000-160673/14.
DR N-PSDB; AAZ98143.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 1; Page 182; 327pp; English.
XX
CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSPP. Antagonists of
CC HSPP are used to treat or prevent disorders associated with increased
CC activity or function of HSPP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
CC nucleic acids can be used for the recombinant production of HSPP, for
CC detecting HSPP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSPP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSPP
CC from natural sources.
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 461; DB 21; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQSLICGGLLAIAAGIAAVLSGK 60
Db 1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQSLICGGLLAIAAGIAAVLSGK 60

QY 61 CKYKSSQKQHSVPPEKAIPLITPGSATTC 89
Db 61 CKYKSSQKQHSVPPEKAIPLITPGSATTC 89